

GenCore version 4.5  
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## OM nucleic - nucleic search, using sw model

Run on: August 25, 2002, 04:18:20 ; Search time 1817.87 Seconds  
(without alignments)  
12340.402 Million cell updates/sec

Title: US-09-811-118-2

Perfect score: 1072  
Sequence: 1 GAGCGCGCCACCTCCGGAAC.....TTGCATCAACATGATTTTC 1072Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

GenEmbl: \*  
1: gb\_da: \*  
2: gb\_htg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*  
15: em\_da: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*  
29: em\_vl: \*  
30: em\_htg\_hum: \*  
31: em\_htg\_inv: \*  
32: em\_htg\_other: \*  
33: em\_htgo\_inv: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
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1	1072	100.0	1072	6	AR151077	AR151077 Sequence
2	1067.2	99.6	1228	9	AK027683	AK027683 Homo sapi
3	1067.2	99.6	1511	6	AX188360	AX188360 Sequence
4	1064.2	99.3	1227	6	AX080813	AX080813 Sequence
5	1035.4	96.6	1251	6	AX080809	AX080809 Sequence
6	809.2	75.5	857	9	AF091092	AF091092 Homo sapi
7	645.4	60.2	160066	2	AL356576	AL356576 Homo sapi
8	473	44.1	1033	10	BC003228	BC003228 Mus muscu
9	435.4	40.6	51381	2	AF322456	AF322456 Homo sapi
10	406.2	37.9	751	6	AX186595	AX186595 Sequence
11	356	33.2	468	6	AX187668	AX187668 Sequence
12	261.8	24.4	51381	2	AF322456	AF322456 Homo sapi
13	217	20.2	241048	2	AL627238	AL627238 Mus muscu
14	177.2	16.5	1047	10	BC019664	BC019664 Mus muscu
15	174.6	16.3	55891	2	AC022847	AC022847 Homo sapi
16	125	11.7	164683	2	AC097883	AC097883 Rattus no
17	115.4	10.8	164683	2	AC097883	AC097883 Rattus no
18	106.2	9.9	9970	1	AE004709	AE004709 Pseudomon
19	106	9.9	203050	1	AE005847	AE005847 Caulobact
20	105.4	9.8	10886	1	AE005847	AE005847 Caulobact
21	104.8	9.8	151813	2	AC026737	AC026737 Homo sapi
22	104.8	9.8	171307	2	AL355820	AL355820 Homo sapi
23	104.8	9.8	176507	2	AC025790	AC025790 Homo sapi
24	104.8	9.8	183494	9	AC091977	AC091977 Homo sapi
25	99.4	9.3	915	8	HV0238745	HV0238745 Homo sapi
26	98	9.1	13404	2	AF322452	AF322452 Homo sapi
27	97.2	9.1	881	8	MCR250951	MCR250951 Mesembrya
28	93.6	8.7	13404	2	AF322452	AF322452 Homo sapi
29	91.6	8.5	701	3	SCMG1UPR	SCMG1UPR Schistosoma
30	91.4	8.5	984	8	AB009083	AB009083 Chlamydom
31	90.2	8.4	890	8	AF242650	AF242650 Hevea bra
32	90	8.4	40969	1	SCD6	SCD6 Streptomy
33	90	8.4	196050	1	AL646058	AL646058 Ralstonia
34	89.6	8.4	1026	8	HV0238697	HV0238697 Hordeum v
35	89.2	8.3	363	11	G71688	G71688 Arabidopsis
36	89.2	8.3	921	8	OSR270955	AJ270955 Oryza sat
37	86.4	8.1	26383	2	AC020674	AC020674 Mus muscu
38	84.4	7.9	3169	1	EC000266	EC000266 Escherich
39	84.4	7.9	10558	1	AE000266	AE000266 Escherich
40	84.4	7.9	10561	1	AE005394	AE005394 Escherich
41	84.4	7.9	19031	1	D90814	D90814 E. coli geno
42	84.4	7.9	19273	1	D90813	D90813 E. coli geno
43	84.4	7.9	257071	1	AP002558	AP002558 Pseudomon
44	84.2	7.9	10647	1	AE004518	AE004518 Pseudomon
45	83.4	7.8	871	8	AF322903	AF322903 Rhipanus

## ALIGNMENTS

RESULT 1	AR151077	1072 bp	DNA	linear	PAT 08-AUG-2001
LOCUS	AR151077	Sequence 2 from patent US 6231853.			
DEFINITION	AR151077	GI:15117127			
ACCESSION	AR151077.1	GI:15117127			
VERSION	AR151077.1	GI:15117127			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1072)				
AUTHORS	Hillman, J. L., Corley, N. C. and Patterson, C.				
TITLE	Human glutathione peroxidase-6				
JOURNAL	Patent: US 6231853-A 2 15-MAY-2001.				
FEATURES	Location/Qualifiers				
source	1..1072				
BASE COUNT	275 a 294 c 270 g 233 t				
ORIGIN	/Organism="unknown"				

Query Match 100.0%; Score 1072; DB 6; Length 1072;  
Best Local Similarity 100.0%; Pred. No. 3.2e-231;





Dh 1056 GAACCTCTGGCCCAATGAGAGCTCTTGACCACTGATCACCAGCCGATAGAGACGTCTG 1115  
Qy 841 CAACAAAATGTGTGGCAATAGACTATATCAAGCAATATCTCCACCCAGGCTTC 900  
Dh 1116 CAACAAAATGTGTGGCAATAGACTATATCAAGCAATATCTCCACCCAGGCTTC 1175  
Qy 901 GTAACTGGGACCAATGATTAATCTATAGGCTGTGTGAGATTAGATGAATACCTG 960  
Dh 1176 GTAACTGGGACCAATGATTAATCTATAGGCTGTGTGAGATTAGATGAATACCTG 1235  
Qy 961 TGAAGTGCCTAGAGAGAGTGCAGCCAAATAGAGGCAATCAATGAATTTTTCATAT 1020  
Dh 1236 TGAAGTGCCTAGAGAGTGCAGCCAAATAGAGGCAATCAATGAATTTTTCATAT 1295  
Qy 1021 AAACCAAAAATTAATCTGTATCAATTAATACTTGATCCACATGATTTTC 1072  
Dh 1296 AAACCAAAAATTAATCTGTATCAATTAATACTTGATCCACATGATTTTC 1347

RESULT 4  
AX080813 1227 bp DNA linear PAT 27-FEB-2001  
LOCUS AX080813 Sequence 59 from Patent WO0109327.  
ACCESSION AX080813  
VERSION AX080813.1 GI:13169783  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 1227)  
Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Klavan, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Pitti, R.M.,  
Matarabe, C.K. and Wood, W.I.  
Method of preventing the injury or death of retinal cells and  
treating ocular diseases  
Patent: WO 0109327-A 59 08-FEB-2001;

TITLE  
JOURNAL  
FEATURES  
source location/Qualifiers  
1. 1227  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 331 a 325 c 293 g 278 t  
ORIGIN

Query Match 99.3%; Score 1064.2; DB 6; Length 1227;  
Best Local Similarity 99.7%; Pred. No. 1.8e-229;  
Matches 1066; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCCGCCACCTCCGAGACAGCATGTTGGCGGCGAGCGTGGCAGCGGCGTGGCTCTCT 63  
Dh 12 GCCGCCACCTCCGAGACAGCATGTTGGCGGCGAGCGTGGCAGCGGCGTGGCTCTCT 71  
Qy 64 GTGGGCTTGGCGGCGGCGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 123  
Dh 72 GTGGGCTTGGCGGCGGCGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 131  
Qy 124 CGCGGCGCAAACTGTGTGCTGAGAGATCCGCGGATCGGTGTCTCCGTGTGTGAATGT 183  
Dh 132 CGCGGCGCAAACTGTGTGCTGAGAGATCCGCGGATCGGTGTCTCCGTGTGTGAATGT 191  
Qy 184 GGGCAGCAGTGGGCGGCTTACAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 243  
Dh 192 GGGCAGCAGTGGGCGGCTTACAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 251  
Qy 244 CCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 303  
Dh 252 CCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 311  
Qy 304 GCGTGACAGCAAGAGATTTGAGAGCTTGGCTGCGGCGCAGCTTACAGATGCTCATTTCC 363  
Dh 312 GCGTGACAGCAAGAGATTTGAGAGCTTGGCTGCGGCGGCGCAGCTTACAGATGCTCATTTCC 371

Qy 364 CATGTTAGCAGATGTCAGTCCAGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 423  
Dh 372 CATGTTAGCAGATGTCAGTCCAGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 431  
Qy 424 CCAGACTTGTGGAGAGAGCCAGCTGGAACCTTGTGAAGTACTGATGAGCCCGAGATGG 483  
Dh 432 CCAGACTTGTGGAGAGAGCCAGCTGGAACCTTGTGAAGTACTGATGAGCCCGAGATGG 491  
Qy 484 AAGGTGTGAGGGGCTTGGAGCCAGCTGTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGG 543  
Dh 492 AAGGTGTGAGGGGCTTGGAGCCAGCTGTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGG 551  
Qy 544 AGCGCTGTGAGGAGAGCTATCTACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 603  
Dh 552 AGCGCTGTGAGGAGAGCTATCTACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 611  
Qy 604 CCTCCACACCTCATCCCGCCAGCTGTGTGGGCTGACCAATGCAAACTCAATATGTCG 663  
Dh 612 CCTCCACACCTCATCCCGCCAGCTGTGTGGGCTGACCAATGCAAACTCAATATGTCG 671  
Qy 664 TTCAAGGGAGAGAGCCAGCTCTCTCTTACTGATGAGGAGGAGGAGGAGGAGGAGGAG 723  
Dh 672 TTCAAGGGAGAGAGCCAGCTCTCTCTTACTGATGAGGAGGAGGAGGAGGAGGAGGAG 731  
Qy 724 TCTTGTGGGGGAAAAATTTAGTATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 783  
Dh 732 TCTTGTGGGGGAAAAATTTAGTATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 791  
Qy 784 CTCTGTGGCAATAGAGCTTGTACAGAGTAAACAGAGGAGGAGGAGGAGGAGGAGGAG 843  
Dh 792 CTCTGTGGCAATAGAGCTTGTACAGAGTAAACAGAGGAGGAGGAGGAGGAGGAGGAG 851  
Qy 844 CAAAATGTGTGGCAATAGAGTATATCAAGCAATATCTCCACCCAGAGGCTTGTGA 903  
Dh 852 CAAAATGTGTGGCAATAGAGTATATCAAGCAATATCTCCACCCAGAGGCTTGTGA 911  
Qy 904 AACTGGAGCAATGATTAATCTCATAGGCGTGTGTGAGGATTTAGATGAATATCTGTGA 963  
Dh 912 AACTGGAGCAATGATTAATCTCATAGGCGTGTGTGAGGATTTAGATGAATATCTGTGA 971  
Qy 964 AAGTGCCTAGGAGAGTGCAGCCAAATAGAGGATTCATGAATTTTGGCATTAATA 1023  
Dh 972 AAGTGCCTAGGAGAGTGCAGCCAAATAGAGGATTCATGAATTTTGGCATTAATA 1031  
Qy 1024 CAAAATAATTAATCTTGTATCAATTAATACTTGATCCACATGAATTTTC 1072  
Dh 1032 CAAAATAATTAATCTTGTATCAATTAATACTTGATCCACATGAATTTTC 1080

RESULT 5  
AX080809 1251 bp DNA linear PAT 27-FEB-2001  
LOCUS AX080809 Sequence 55 from Patent WO0109327.  
DEFINITION AX080809  
ACCESSION AX080809  
VERSION AX080809.1 GI:13169779  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 1251)  
AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Klavan, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Pitti, R.M.,  
Matarabe, C.K. and Wood, W.I.  
Method of preventing the injury or death of retinal cells and  
treating ocular diseases  
Patent: WO 0109327-A 55 08-FEB-2001;  
JOURNAL Genentech, Inc. (US)  
FEATURES  
source location/Qualifiers  
1. 1251  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Partial DNA sequence used to isolate DNA57037."

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unsure 1231
      /note="unknown base"
BASE COUNT 343 a 328 c 298 g 280 t 2 others
ORIGIN
Query Match 96.6%; Score 1035.4; DB 6; Length 1251;
Best Local Similarity 99.4%; Pred. No. 5.7e-223;
Matches 1069; Conservative 1; Mismatches 2; Indels 3; Gaps 3;

QY 1 GAGCGCGCCACCTCCGGCAACAGCCATGGTGGGCGGAGCGTGGGACGGCGCGTGGCTGT 60
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Db 4 GAGCGCGCCACCTCCGGCAACAGCCATGGTGGGCGGAGCGTGGGACGGCGCGTGGCTGT 63
QY 61 CCTGTGGGCTGGGCGCTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
   |||||||
Db 64 CCTGTGGGCTGGGCGCTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
QY 121 CATCCGGGGCAAACTGTGTGCTGAGAGAAATACCGCGGATCGGTGTCCCTGGTGGTGA 180
   |||||||
Db 124 CATCCGGGGCAAACTGTGTGCTGAGAGAAATACCGCGGATCGGTGTCCCTGGTGGTGA 183
QY 181 TGTGGCCACGAGTGGGCGCTTCACACACGAGCTACCGAGCCCTGACGAGCTGCAGCG 240
   |||||||
Db 184 TGTGGCCACGAGTGGGCGCTTCACACACGAGCTACCGAGCCCTGACGAGCTGCAGCG 243
QY 241 AGACCTGGGCGCCCGCCACCTTCAAGCTGCGCTTCCCTGCACACGAGTTGGCCACAC 300
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Db 244 AGACCTGGGCGCCCGCCACCTTCAAGCTGCGCTTCCCTGCACACGAGTTGGCCACAC 303
QY 301 GGAGCTGACAGCAGACAGAGAGATGAGAGCTTTGGCTGCCGACCTACAGTGTGTC-TCAT 359
   |||||||
Db 304 GGAGCTGACAGCAGACAGAGAGATGAGAGCTTTGGCTGCCGACCTACAGTGTGTCAT 363
QY 360 TCCCGCATGTTTA-GCAAGATGAGTACCGGAGT-GGTGGCCATGCTCCCTTCAAGTA 417
   |||||||
Db 364 TCCCGCATGTTTAAGCAAGATGAGTACCGGAGTGGGCGCCATGCTCCCTTCAAGTA 423
QY 418 CCTGGCCACGAGCTTGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 477
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Db 424 CCTGGCCACGAGCTTGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 483
QY 478 AGATGAAAGGTGTAGGGGCTTGGAGCCCACTGTGTGAGTGGAGAGTACAGACTCCA 537
   |||||||
Db 484 AGATGAAAGGTGTAGGGGCTTGGAGCCCACTGTGTGAGTGGAGAGTACAGACTCCA 543
QY 538 GATCAGAGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 597
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Db 544 GATCAGAGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 603
QY 598 TCTCTCTCTCACACACCTCATCCGCGCCACCTGTGTGGGCTGACCAATGCAAACTCAA 657
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Db 604 TCTCTCTCTCACACACCTCATCCGCGCCACCTGTGTGGGCTGACCAATGCAAACTCAA 663
QY 658 TGTGCTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 717
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Db 664 TGTGCTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 723
QY 718 CATCATCTTGTGGGGGAAAAATTTAGATTTTGTATTTTGAATTTTGAATTTTGAATTTTGA 777
   |||||||
Db 724 CATCATCTTGTGGGGGAAAAATTTAGATTTTGTATTTTGAATTTTGAATTTTGAATTTTGA 783
QY 778 TAGGAATCTGTGGCGATGAGAGCTTGTGACAGTAATCAGCAGCGATGACAGAGCTGT 837
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Db 784 TAGGAATCTGTGGCGATGAGAGCTTGTGACAGTAATCAGCAGCGATGACAGAGCTGT 843
QY 838 TGTCAACAAAAATGTGTGGCAATAGAGATATCAAGCAATATCTCCACCCAAAGCT 897
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Db 844 TGTCAACAAAAATGTGTGGCAATAGAGATATCAAGCAATATCTCCACCCAAAGCT 903
QY 898 TGTGTAAAGTGGGAGCAATGATTACCTCATAGGGGCTGTGTGAGAGATTAGAGAAATAC 957
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Db 904 TGTGTAAAGTGGGAGCAATGATTACCTCATAGGGGCTGTGTGAGAGATTAGAGAAATAC 963
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QY 958 CTGTGAAAGTGCCTTAGGACAGTGCAGCCAAATAGAGAGCATTCATGAACTTTTGGCA 1017
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QY 1018 TATTAACCAAAAAATATCTGTTATCATATAAAACTTGGATCCCAACATGATTTTC 1072
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Db 1024 TATTAACCAAAAAATATCTGTTATCATATAAAACTTGGATCCCAACATGATTTTC 1078

RESULT 6
AF091092 857 bp mRNA linear PRI 12-NOV-1998
LOCUS Homo sapiens clone 683 unknown mRNA, complete sequence.
DEFINITION AF091092
ACCESSION AF091092.1 GI:3860021
VERSION FLI_CDNA.
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 857)
AUTHORS Barrow,I.K., P., Boguski,M.S., Touchman,J. and Spencer,F.
TITLE Full-insert sequence of mapped XREF EST
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 857)
AUTHORS Barrow,I.K., P., Boguski,M.S., Touchman,J. and Spencer,F.
TITLE Direct Submission
JOURNAL Submitted (31-AUG-1998) NHGRI, NIH, 49 Convent Drive, Building 49,
Room 2C08, Bethesda, MD 20892, USA
FEATURES
source
1..857
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1q24-q41"
/clone="683"
/note="location inferred using conservation of syteny
with mouse locus D1Xrf379"
46..225
/codon_start=1
/product="unknown"
/protein_id="AAC72961.1"
/db_xref="GI:3860022"
/translation="MANRSLTATRRRLAPAPYVSHSPCLARLQSPVLPILPSSWT
PRLGRSPGTSGST"
BASE COUNT 267 a 216 c 184 g 190 t
ORIGIN
Query Match 75.5%; Score 809.2; DB 9; Length 857;
Best Local Similarity 99.6%; Pred. No. 5.2e-172;
Matches 811; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 255 ACCACTTCAAGCTGCTGCGCTTCCCTGCAACAGAGTTGGCCAAAGAGAGCTGACAGCA 314
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Db 10 ACCACTTCAAGCTGCTGCGCTTCCCTGCAACAGAGTTGGCCAAAGAGAGCTGACAGCA 69
QY 315 ACAAGGAGATTGAGAGCTTGGCTGCCGACCTACAGAGTGTGATTTCCCATGTTTAGCA 374
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Db 70 ACAAGGAGATTGAGAGCTTGGCTGCCGACCTACAGAGTGTGATTTCCCATGTTTAGCA 129
QY 375 AGATTGAGTACAGCGGAGTGGTGGCCATCTGCTTCAAGTACAGTACAGTGGCCAGAGCTTCTG 434
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Db 130 AGATTGAGTACAGCGGAGTGGTGGCCATCTGCTTCAAGTACAGTACAGTGGCCAGAGCTTCTG 189
QY 435 GGAAGGAGCCCGACCTGGAAGTGTGAGAGTACTAGTGGCCAGAGTGAAGGTGGTAG 494
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Db 190 GGAAGGAGCCCGACCTGGAAGTGTGAGAGTACTAGTGGCCAGAGTGAAGGTGGTAG 249
QY 495 GGGCTTGGAGCCCACTGTGTGAGTGGAGAGGTCAGAGTTCAGATACAGCGCTGCTGA 554
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[illegible][illegible]

Db 112088 TTGGTGGGGGAAAAATCTTAGTATTTTGATTTATTTGAATCTTACAGCAACAAATAGGAACT 112029

QY 786 CCTGGCCCATGAGAGCTCTTGACACGTAAATCACCAGCCGATAGGAACTCTTGCCAACA 845

Db 112028 CCTGGCCCATGAGAGCTCTTGACACGTAAATCACCAGCCGATAGGAACTCTTGCCAACA 111969

QY 846 AAAATGTGGCAATTAGAGATATATCAAGCAATATCTCCACACCAGGCTCTGTATAA 905

Db 111968 AAAATGTGGCAATTAGAGATATATCAAGCAATATCTCCACACCAGGCTCTGTATAA 111909

QY 906 CTGGGACCAATGATTACCTCATAGGCGCTGTGTGAGATTATAGATGAATACCTGTGAAA 965

Db 111908 CTGGGACCAATGATTACCTCATAGGCGCTGTGTGAGATTATAGATGAATACCTGTGAAA 111849

QY 966 GTGCTTAGGCAATGCTCCAGCCAAATATGAGGCAATTCATGAACATTTTTTGCAATATAAAC 1025

Db 111848 GTGCTTAGGCAATGCTCCAGCCAAATATGAGGCAATTCATGAACATTTTTTGCAATATAAAC 111789

QY 1026 AAAAATTAACGTGTATCAATATAAANCTGCAATCCCAATGAAATTTTC 1072

Db 111788 AAAAATTAACGTGTATCAATATAAANCTGCAATCCCAATGAAATTTTC 111742

RESULT	8
BC003228	
LOCUS	BC003228
DEFINITION	Mus musculus, Similar to RIKEN cDNA 3110050F08 gene, clone MGC:65811
IMAGE:3483448,	mRNA, complete cds.
	1033 bp
	mRNA linear
	ROD 12-JUL-2001

ACCESSION	BC003228	
VERSION	BC003228.1	GI:13096857
KEYWORDS	MGC.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE 1 (bases 1 to 1033)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (20-FEB-2001) National Institutes of Health, Mammalian

REMARK	COMMENT
NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>	Contact: MGC help desk

Address: 5060s Research Triangle  
 Tissue Procurement: Lochter Hennighausen Ph.D., Robin Humphreys  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINI),  
 DNA Sequencing by: Baylor College of Medicine Human Genome  
 Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: villalon@bcm.tmc.edu.  
 Villalon, D.K., Luna, R.A., Hale, S.M., Huylk, S., Lu, X., Garcia,  
 A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,  
 Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
 Series: IRAC Plate: 6 Row: 6 Column: 16  
 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

FEATURES	source	Location/Qualifiers
1..1033		
/organism="Mus musculus"		
/db_xref="taxon:10090"		
/clone="MGC:6581 IMAGE:348348"		
/tissue_type="mammary tumor. WAP-IGF alpha model. 7 months old, gross tissue."		
/clone_11b="NCI-CGAP_Mam5"		
/lab_host="DH10B"		

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/note="Vector: pCMV-SPORT6"
38..598
/codon_start=1
/product="Similar to RIKEN CDNA 3110050F08 gene"
/protein_id="AAH03228.1"
/db_xref="gi:13096858"
/translation="MVAAYATAMLLMNAACQSEQDFYDKAVINIRGLVLSLEKRGK
SVSLVYVAASEGFDQNYRALQOLRGLGHHNVLAFCPCNCGQCEPPTNRLEKRF
ARRIVYVSEPMSEKIAVTCGAAHPAFKYLQTSKEPTWNNWKLVLPDGGVVGAMDP
TVPVAIEKRTIEQYMKLLKRRDL"
BASE COUNT      264 a      285 c      270 g      214 t
ORIGIN

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Query Match	Similarity	44.1%	Score 473	DB 103	Length 1033
Best Local	Similarity	72.2%	Pred. No. 3	le-96	
Matches	723	Conservative	0	Mismatches	220
			Indels	58	Gaps
Oy	2	ACGCCGCACACCTCCGGAACACGACATGATGAGCGGAGCGAGGTGGCAGCGGCGTGCCTC	61		
Db	14	AAGTCCCACTCCCGGAGAGTGAACCAATGTTGTCAG--CTGTGGCAGCGGCGTGCCTC	70		
Oy	62	CTGTGGGCTGGGGCCCTGGCGGCGAGGAGGAGGACCTCTACGACTTCAAGCGGCTCAC	121		
Db	71	CTGTGGGCGCGGCGCTGGCGGCAATCCGAGGACCTTCAAGACTTCAAGCGGCTCAC	130		
Oy	122	ATCCGGGGCAACCTGGTGTCCGTGGAGAAGTACCCCGATCCGTTCCCTGGTGTGAAT	181		
Db	131	ATCCGGGGCAACCTGGTGTCCGTGGAGAAGTACCGGTGGCTGTCCCTGGTGTGAAC	190		
Oy	182	GTGGCCAGCGAGTGGCGCTTCAAGACAGCACTACGAGCCCTGACAGCTGACGGA	241		
Db	191	GTAGCTAGGGAATGTGGCTTCAAGACCGAACTACCGGCTTCAAGCTGACGAGGG	250		
Oy	242	GACCTGGGCGCCACCACTTCAACGTCGCGCTTCCCTGCAACAGTTTGGCCACAG	301		
Db	251	GACCTGGGCGCCCACTTCAATGTGCTTGGCTTCCCTGCAACAGTTTGGCCACAG	310		
Oy	302	GAGCTGCAGACACAGAGATTGAGACTTGTGCTGCGCAGCTTACAGTGTCTCATTC	361		
Db	311	GAACTGCAGACACAGAGATTGAGACTTGTGCTGCGCAGCTTACAGTGTCTCATTC	370		
Oy	362	CCCATTTTGAAGAAGTTCCAGTACCCGCTACTGGGCGCCATCCGCTTCAAGTACCG	421		
Db	371	CCCATTTTGAAGAAGTTCCAGTACCCGCTACTGGGCGCCATCCGCTTCAAGTACCTA	430		
Oy	422	GCCCACTTCTGGGAAGAGGCCAATCTGGAATCTTGGAACTACTAGTACCCCAAT	481		
Db	431	ACCCAGACTTCTGGGAAGAGGCCAATCTGGAATCTTGGAACTACTAGTACCCCAAG	490		
Oy	482	GGAAGGTGTAGGGCTTGGACCACTGTGTCAGTGAGGAGGTCAAGCTCCAGATC	541		
Db	491	GGAAGGTGTGTAGGACATGTGACCACTGTGTCAGTGAGGAGGTCAAGGCTCCGTATT	550		
Oy	542	ACAGCCCTGTGAGGAAGTCACTCACTGGAAGCGAGAACTTATTAACCAACGCGGTCTC	601		
Db	551	ACAGAGCAGAGTGTGAATCACTCTCGGAACGAGAACTTGTGTAC-----	599		
Oy	602	CTTCCTCACACCTCATCCGCCCACTGTGTGGGCTGACCAATGCACAACTCAATGCT	661		
Db	600	-----CGGTCCCTTGGAACTCCCATCCCTCGCAACTCAAGTGT	642		
Oy	662	GCTTCAAGAGGAGACCCACGTGACTCTCTCTCTTACTCTTATGCCATTGTGCCATTC	721		
Db	643	GCTTCAAGAGGAGGAGGCTTAAAGCTTCTCTCTCTTCACTCT-----	685		
Oy	722	ATTCCTGTGGGAAAAATCTAGTATTTTGAATATTTGAATCTTACAGCACAATAGG	781		
Db	686	-----CAGAGCAAAATCTTAAGACTTGGATGATTTAATTCGAAGCAACGAGACAGC	738		
Oy	782	AACCTCTGGCAATGAGACTCTTGACCAAGTAAATACAGCCGATTA--CGAAGCTTGTG	840		
Db	739	AACCTCTCTGGCAATGAGACTCTTAAACAGCAATATACAGCCAGGCGGCGCTTGTAGC	798		

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* 21889 22072: contig of 184 bp in length
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* 22073 22788: contig of 716 bp in length
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* 22789 23448: contig of 660 bp in length
* gap of unknown length
* 23449 23658: contig of 210 bp in length
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* 23870 24449: contig of 580 bp in length
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* 24450 25107: contig of 658 bp in length
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* 29981 30204: contig of 224 bp in length
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* 30726 31377: contig of 652 bp in length
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* 31378 31587: contig of 210 bp in length
* gap of unknown length
* 31588 31792: contig of 205 bp in length
* gap of unknown length
* 31793 32403: contig of 611 bp in length
* gap of unknown length
* 32404 33056: contig of 653 bp in length
* gap of unknown length
* 33057 33266: contig of 210 bp in length
* gap of unknown length
* 33267 33471: contig of 205 bp in length
* gap of unknown length
* 33472 34137: contig of 666 bp in length
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* 34138 34789: contig of 652 bp in length
* gap of unknown length
* 34790 35003: contig of 214 bp in length
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Best Local Similarity 40.6%; Score 435.4; DB 2; length 51381;
88.1%; Pred. No. 1.4e-87;
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QY 136 GGTGCGCTGGAGAACTACCGCGGATCGGTCGCCGTGGTGAATGTGGCCAGAGTG 195
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Db 50834 GGTGCGCTGGAGAACTACCGCGGATCGGTCGCCGTGGTGAATGTGGCCAGAGTG 50893
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Db 50894 CGGCTTCACAGACACAGACTACCGAGCCCTGCAGCAGTGCAGCGAGAGCTGGGCCCA 50953
QY 256 CCACCTCAACGTGCTGCGCTTCCCTCGCAACAGTTGGCCAAAGAGAGCTGCAGCA 315
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Db 50954 CCACCTCAACGTGCTGCGCTTCCCTCGCAACAGTTGGCCAAAGAGAGCTGCAGCA 51013
QY 316 CAAGGAGATTGAGAGCTTGGCCCGGACCTACAGTGTCTATTCGCCATGTTAGCA 375
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Db 51014 CAAGGAGATTGAGAGCTTGGCCCGGACCTACAGTGTCTATTCGCCATGTTAGCA 51073
QY 376 GATTGAGTCAACGCTGACTGCTGCTCCATCCCTCAAGTACCTGGCCAGACTTCTGG 435
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Db 51074 GATTGAGTCAACGCTGACTGCTGCTCCATCCCTCAAGTACCTGGCCAGACTTCTGG 51133
QY 436 GAAGAGCCCACTGGAACCTTGTGAAGTACCTAGTACCCCAAGAGAAAGGTGATAG 495
|||||
Db 51134 GAAGAGCCCACTGGAACCTTGTGAGAGTCTAATTAACCAATGAGAGGTGATAG 51193
QY 496 GCGTGGAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAG 555
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Db 51194 GCGTGGAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAG 51253
QY 556 GAAGCTCATCTCTACTGAAGAGAGAGTATTAACCAAGCGCTGCTGCTGCTGCTGAG 615
|||||
Db 51254 GAAGCTCATCTCTACTGAAGAGAGAGTATTAACCAAGCGCTGCTGCTGCTGAG 51312
QY 616 CATCCCGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAG 675
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Db 51313 CATCCCGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAG 51372
QY 676 GACCCACT 683
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Db 51373 GACCCACT 51380
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RESULT 10
AX186595/c 751 bp DNA linear PAT 06-AUG-2001
LOCUS
DEFINITION Sequence 2290 from Patent WO0142467.
ACCESSION AX186595
VERSION AX186595.1 GI:15138034
KEYWORDS
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 751)
AUTHORS Schlegel,R., Deeds,J., Berger,A. and Zhao,X.
TITLE Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
JOURNAL Patent: WO 0142467-A 2290 14-JUN-2001.
Milelennium Predictive Medicine, Inc. (US)
FEATURES
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1..751
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/db_xref="taxon:9606"
BASE COUNT 194 a 141 c 143 g 269 t 4 others
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Best Local Similarity 37.9%; Score 406.2; DB 6; length 751;
Matches 419; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 650 AACTCAATGTCCTTCAAGGAGAGACCCACTGACTCTCTCTTACTCTATGCC 709
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QY	770	GCACAAATAG GAACCTCTGSC CAATGAGCTCT TGACCACTGAT CACCAGCCGAT AC	829	
Db	626	GCACAAATAG GAACCTCTGSC CAATGAGCTCT TGACCACTGAT CACCAGCCGAT AC	567	
QY	830	GACGTCCTTGC CACAAAATGTG TGGCAATTAGA AGATATCAAGC AAATATCTCCAC	889	
Db	566	GACGTCCTTGC CACAAAATGTG TGGCAATTAGA AGATATCAAGC AAATATCTCCAC	507	
QY	890	CCAAAGCTTCT GTAACTGGGAC CAATGATTAAC CATAGGGCTGT GTGAGGATTAGA	949	
Db	506	CCAAAGCTTCT GTAACTGGGAC CAATGATTAAC CATAGGGCTGT GTGAGGATTAGA	447	
QY	950	TGAATTAACCT GTGAAGTGCTT AGGACAGGCCA AGCAATAGSAG CGCATTCATGA CAT	1009	
Db	446	TGAATTAACCT GTGAAGTGCTT AGGACAGGCCA AGCAATAGSAG CGCATTCATGA CAT	387	
QY	1010	TTTTTGCATTA TAAACAAAAAT TACTTGTATCA TATAAAACTTG CATCCACATGAT	1069	
Db	386	TTTTTGCATTA TAAACAAAAAT TACTTGTATCA TATAAAACTTG CATCCACATGAT	327	
QY	1070	TTC	1072	
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RESULT	11
AXI87668/c	
LOCUS	AXI87668 468 bp DNA linear PAT 06-AUG-2001
DEFINITION	Sequence 3363 from Patent WO0142467.
ACCESSION	AXI87668
VERSION	AXI87668.1 GI:15139132
KEYWORDS	.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 468) Schlegel,R., Deeds,J., Berger,A. and Zhao,X. Genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of cervical cancer Patent: WO 0142467-A 3363 14-JUN-2001; Millennium Predictive Medicine, Inc. (us)
JOURNAL	
FEATURES	Location/Qualifiers
SOURCE	1..468 /organism="Homo sapiens" /db_xref="taxon:9606"
BASE COUNT	131 a 84 c 94 g 159 t
ORIGIN	

Query Match	33.2%;	Score 356;	DB 6;	Length 468;
Best Local Similarity	100.0%;	Pred. No. 6.6e-70;		
Matches 356;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	717	CCATCATCTCTGTGGGGGAAAAAATTCTAGATATTTGATTTATTGTAACCTTACAGCAACA	776
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QY	777	ATGGAACCTCTGGCGCATGAGACCTCTTGACCGATAATCACAGCGGATACGAAGCTC	836
Db	408	ATAGGAACCTCTGGCGCATGAGACCTCTTGACCGATAATCACAGCGGATACGAAGCTC	349
QY	837	TTGGCCAAACAAAATGTGTGGCAATAGAGATATTCAAAGCAATATCTCCACCCAAAGC	896
Db	348	TTGGCCAAACAAAATGTGTGGCAATAGAGATATTCAAAGCAATATCTCCACCCAAAGC	289

Qy	897	TTTCGTAACTGGGACCAATGATTAACCTCAATAGGGCGTGTGGAGATTTGAGATGAATA	956
Db	288	TTTCGTAACTGGGACCAATGATTAACCTCAATAGGGCGTGTGTGAGATTTGAGATGAATA	229
Qy	957	CCTGTGAAGTGCCTTAGGCATGCGCAGCCAAATATGAGGGCATTCATAGCAATTTTTCG	1010
Db	228	CTGTGGAAGTGCCTTAGGCATGCGCAGCCAAATATGAGGGCATTCATAGCAATTTTTCG	169
Qy	1017	ATATTAACCAAAAATAATCTGTTATCATTAATAAATTCGCATCCACATGAAATTC	1072
Db	168	ATATTAACCAAAAATAATCTGTTATCATTAATAAATTCGCATCCACATGAAATTC	113

RESULT	12
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LOCUS	AF322456
DEFINITION	51381 bp DNA linear HTG 06-DEC-2000
	Homo sapiens chromosome 17 clone BAC629P10 map 1P13.3, ***
ACCSSION	AF322456
VERSION	AF322456
KEYWORDS	HTG; HTGS_PHASE1.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	1 (bases 1 to 51381)
AUTHORS	Zhao,X.T., He,M., Wan,D.F., Ye,Y., Qin,W.X., Huang,Y., Zuo,L. and Gu,J.X.
TITLE	Gene clone on human chromosome 17p13.3
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 51381)

**TITLE** Direct Submission  
**JOURNAL** Submitted (21-NOV-2000) National Laboratory for Oncogenes & Related Genes, Shanghai Cancer Institute, 25/In 2200 Xie-Tu Road, Shanghai 200032, P. R. China  
**COMMENT** \* NOTE: This is a 'working draft' sequence. It currently

COMMENT

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 120 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

*	1	236:	contig of 236 bp in length
*			gap of unknown length
*	237	435:	contig of 199 bp in length
*			gap of unknown length
*	436	665:	contig of 230 bp in length
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*	666	879:	contig of 214 bp in length
*			gap of unknown length
*	880	1121:	contig of 242 bp in length
*			gap of unknown length
*	1122	1948:	contig of 827 bp in length
*			gap of unknown length
*	1949	2628:	contig of 680 bp in length
*			gap of unknown length
*	2629	3229:	contig of 601 bp in length
*			gap of unknown length
*	3230	3893:	contig of 664 bp in length
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*	3894	4090:	contig of 197 bp in length
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*	4634	5219:	contig of 586 bp in length
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\* 6119 6334: contig of 216 bp in length  
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\* 6485 6623: contig of 139 bp in length  
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\* contig of 652 bp in length  
\* 34790 35003: gap of unknown length  
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Query Match 24.4%; Score 261.8; DB 2; length 51381;  
Best Local Similarity 80.3%; Pred. No. 1.9e-48;  
Matches 380; Conservative 0; Mismatches 87; Indels 6; Gaps 6;

QY 604 CTTCCACCACTTCATCCCGCCACCTGTGTGGGCTGACCAATGCAACCAATGCTGC 663  
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QY 664 TTCAAAAGGAGAGAC-CCACTGACTCTCTTCC-TTACTCTTATGCCAT-TGCTCCCAT 720  
DB 21407 TTCAAAAGGAGAGACCTCCATGCTCTCTTCCGTTTACTTATGACATGTGTCCAT 21348  
QY 721 CATCTTGTGTGGGAAA-AATTCATGATTTTGTATTTGATCTTACGACCAATA 779  
DB 21347 CAATCTGTGTGGGAAAATGTTGATGATTTGATTTTAACTTTACATCCACACATA 21288  
QY 780 GGAATCTCTGAGCAATGAGACTCTTGACCAATGATCCAGCCGATGACAGCTCTTG 839  
DB 21287 GGGACATGATCCATGATGAAAGGTCGTATGATGATTCACCATCCGATGAGGAGCTTCT 21228  
QY 840 CCAACAAAATGTGTGGCAATAGAAATATATCAAGCAATATCTCCACCAAGCTTC 899  
DB 21227 GCATCAAAAATGTGTGGCAATATATGATATATCAAGCTATAGTCT-TCACACAAAGCTTC 21169  
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DB 21168 TGTAAATCT-GTACCAATGTTTACCTCATAGGCTGTGTGATGATGATCAAAATACCT 21110  
QY 960 GTGAAAGTGCCTAGGAGAGTCCAGCAATAGGAGGATTCATGATGATTTTGCATA 1019  
DB 21109 GTGAAATGCTCTAGGAGAGTCCAGCAATAGGAGGATTCATGATGATTTTGCATA 21050  
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DB 21049 TAAATCCAAAAGATPACTGTTATCAATAAAACTTGATCCACATGATTTTC 20997

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HTG: HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULFILLTOP.  
SOURCE  
MUS musculus  
house mouse.  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (sites)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Sims,S.  
Direct Submission  
Submitted (30-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
requests: clonerequest@sanger.ac.uk  
On Nov 1, 2001 this sequence version replaced gi:16580350.  
----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquerry@sanger.ac.uk  
----- Project Information  
Center project name: DM46M23  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: plasmid; 108752; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Consensus quality: 238381 bases at least Q40  
Consensus quality: 238827 bases at least Q30  
Consensus quality: 239150 bases at least Q20  
Insert size: 239848; sum-of-contigs  
Insert size: 228542; 2.6% error; agarose-fp  
Quality coverage: 8.48x in Q20 bases; sum-of-contigs Quality  
coverage: 10.79x in Q20 bases; agarose-fp  
\* NOTE: This is a 'working draft' sequence.

\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved

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Matches 238; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 163 GGTGTCCTGCTGTGATGTGGACGAGTGGGCTTGCAGACGACGACTACGAGC 222  
DB 135078 GGTTCCTGCTGTGATGTGGACGAGTGGGCTTGCAGACGACGACTACGAGC 135019  
QY 223 CTTGCACAGCTGAGGAGACCTGGGCCCCCAACCACTTCAACGTGCTCCCTCTG 282  
DB 135018 CTTGCACAGCTGAGGAGACCTGGGCCCCCAACCACTTCAACGTGCTCCCTCTG 134959  
QY 283 CAACCACTTTGGCCACAGAGACCTGACAGCAACAGAGATTTGAGCTTTGCCCTGCCG 342  
DB 134958 CAACCACTTTGGCCACAGAGACCTGACAGCAACAGAGATTTGAGCTTTGCCCTGCCG 134899  
QY 343 CACCTACAGTGTCTATCCCATGTTTACAGATTTGACAGGATGACGAGTACTGCTGCCCA 402  
DB 134898 CACCTACAGTGTCTATCCCATGTTTACAGAGATGACGAGTACTGCTGCCCA 134839

OY 403 TCCTGCTTCAAGTACCTGGCCAGACTTCTGG 435  
 DB 134838 CCTGCTTCAAGTACCTAACCCGTGAGTCTTG 134806  
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 BC019664  
 LOCUS  
 DEFINITION Mus musculus, RIKEN cDNA 2310016C16 gene, clone MGC:30772  
 ACCESSION BC019664  
 VERSION BC019664.1 GI:18044309  
 KEYWORDS  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1047 bp mRNA linear ROD 22-JAN-2002  
 IMAGE:3988837, mRNA, complete cds.  
 REFERENCE  
 1 (bases 1 to 1047)  
 Strausberg, R.  
 Direct Submission  
 Submitted (19-DEC-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: http://mgc.nci.nih.gov  
 Contact: MGC help desk  
 Email: cgaabbs-remail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLU)  
 DNA Sequencing by: Baylor College of Medicine Human Genome  
 Sequencing Center  
 Center code: BCM-HGSC  
 Web site: http://www.hgsc.bcm.tmc.edu/cdna/  
 Contact: amgebcm.tmc.edu  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Huiy, S.W., Hale, S.M.,  
 Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,  
 Richards, S., Gibbs, R.A.  
 Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/ILLU at: http://image.llnl.gov  
 Series: IRAC Plate: 40 Row: 1 Column: 9  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: Hexamer frequency ORF  
 analysis.  
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 DB 150 CTTTACTCTCTTGAAGTAAAGATGCCAAGAGAACCGCTGTCTGTGAAAAGTTCA 209  
 OY 157 CGGATCGGTGTCCTGTGTGTGATGTGGCCAGGAGTGGGCTTCACAGCCAGCACTA 216  
 DB 210 AGGCAAGGCTTCCCTGGTGTGAACGTCGTAGTGCCTCCGCTCACAGCAAGAGTTA 269  
 OY 217 CCGAGCCCTGACAGAGCTGACGAGACTGGGCCCCCAGCACTTCAGCTGCGCTT 276  
 DB 270 CCAGATTCTCAAGGAGCTACACAGAGATTGGGCTTCATCTTCAAGTCTGCGCTT 329  
 OY 277 CCCCTGACAGCGTTGGCCACAGAGGCTTCACAGCAAGGAGATGAGAGCTTTTC 336  
 DB 330 CCCGTGCAATCAGTTTGGGAAATCGGAGCCCAAGTCCAGCAAGGAGATGAAATCTTTTC 389  
 OY 337 CTTCCGACCTACAGTGTCTCATTTCCCAATGTTTGAAGATTTGACACCGTACTGG 396  
 DB 390 GAGACGAGACTACGAGGTACATTCCTCCCAAGATTAAGATTAGAGGCGCGGA 449  
 OY 397 TGGCCATCTGCTTCAAGTACCTGAGCCAGACTTCTGGGAAGAGACCACTGAGACTT 456  
 DB 450 AGCAGAACCTGGCTTGAATTTATGTTGATCTTCCAAAGAGAGCCAGGTGGAATTT 509  
 OY 457 CTGGAAGTACTAGTAGAGCCCAAGTGAAGGTGGTGGGCTGGAGCCCAACTGTGTC 516  
 DB 510 TTGGAAAGTATCTGGTCAACCTGAGGACAGTCTGGAAGTCTGGAGGCCAGGAAGACC 569  
 OY 517 AGTGAAGAGGTGACAGCTCAGATCAGACAGCGCTGTGAGGAAGCTCATCTGTAAGCG 576  
 DB 570 CCTTGAAGCCATCAGACCTCATGTATCAAAATGATTGGCAAAATATCTTAAAAAGAA 629  
 OY 577 AGAAGACTATATACCAACCCGCT 598  
 DB 630 AGAGGATCTATGAACCAACCCGCT 651  
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 ACCESSION AC022847  
 VERSION AC022847.1 GI:6922212  
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 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 55891)  
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
 Homo sapiens chromosome 11, clone RP11-261F7  
 Unpublished  
 2 (bases 1 to 55891)  
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,  
 Anderson, S., Baldwin, J., Barna, N., Beckler, R., Bedalov, F.,  
 Boguslavsky, L., Bouhgalter, B., Brown, A., Burkett, G., Castle, A.,  
 Choquet, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,  
 DeArrellano, K., Dewar, K., Domino, M., Doyle, M., Fensholt, J.,  
 Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,  
 Gardina, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
 Howland, J. C., Johnson, R., Jones, C., Kahn, L., Karatas, A., Klein, J.,  
 Lander, T., Lechoczky, J., Levine, R., Liu, C., Liu, G., Locke, K.,  
 Macdonald, P., Marquis, N., McEwan, P., McKusick, A., McKernan, K.,  
 McPherson, R., Melchior, J., Menus, L., Morrow, J., Naylor, J.,  
 Norman, C. H., O'Connor, T., O'Donnell, P., Olivari, T. M., Peterson, K.,  
 Piere, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,  
 Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,  
 Stojanovic, N., Subramanian, A., Talamas, J., Testa, S., Theodore, J.,  
 Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,  
 Zimmer, A. and Zody, M.  
 Direct Submission

JOURNAL  
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smt, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

----- Project Information  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
Project name: 16164

Center clone name: 261\_F\_7

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\* NOTE: This record contains 78 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 698: contig of 698 bp in length  
\* 699 1436: contig of 738 bp in length  
\* 1437 2155: contig of 719 bp in length  
\* 2156 2866: contig of 711 bp in length  
\* 2867 3559: contig of 693 bp in length  
\* 3560 4266: contig of 707 bp in length  
\* 4267 4955: contig of 689 bp in length  
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\* 5657 6372: contig of 716 bp in length  
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\* 7083 7807: contig of 725 bp in length  
\* 7808 8527: contig of 720 bp in length  
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\* 9954 10663: contig of 710 bp in length  
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\* 11393 12092: contig of 700 bp in length  
\* 12093 12805: contig of 713 bp in length  
\* 12806 13523: contig of 718 bp in length  
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\* 16428 17145: contig of 718 bp in length  
\* gap of unknown length

\* 17146 17851: contig of 706 bp in length  
\* 17852 18565: contig of 714 bp in length  
\* 18566 19394: contig of 828 bp in length  
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\* 20113 20839: contig of 727 bp in length  
\* 20840 21558: contig of 719 bp in length  
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\* 22285 23015: contig of 731 bp in length  
\* 23016 23739: contig of 724 bp in length  
\* 23740 24445: contig of 706 bp in length  
\* 24446 25157: contig of 712 bp in length  
\* 25158 25859: contig of 702 bp in length  
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\* 26567 27276: contig of 710 bp in length  
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QY	428	ACTTCTGGG	436
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